

SEQUENCE LISTING

<110> Molero, Juan C  
James, David  
  
<120> Methods of treatment of feeding disorders or disorders of glucose  
uptake and for modifying metabolism and identifying therapeutic  
reagents therefor  
  
<130> 42-000200US  
  
<140> US 10/539,105  
<141> 2005-06-14  
  
<150> AU 2002953393  
<151> 2002-12-16  
  
<150> AU 2003906285  
<151> 2003-11-14  
  
<150> PCT/AU2003/001676  
<151> 2003-12-16  
  
<160> 261  
  
<170> PatentIn version 3.3  
  
<210> 1  
<211> 153  
<212> PRT  
<213> artificial  
  
<220>  
<223> disrupted mouse Cbl protein  
  
<400> 1

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Ser  
1 5 10 15

Gly Gly Ser Gly Ala Gly Gly Leu Ile Gly Leu Met Lys Asp Ala Phe  
20 25 30

Gln Pro His His His His His Leu Ser Pro His Pro Pro Cys Thr  
35 40 45

Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp Lys Val  
50 55 60

Val Arg Leu Cys Gln Asn Pro Asn Val Ala Leu Lys Asn Ser Pro Pro  
65 70 75 80

Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg Thr Val  
85 90 95

Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn Glu Tyr  
100 105 110

Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln Thr Ile  
115 120 125

Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn Ser Gln  
130 135 140

Pro Arg Arg Asn Leu Thr Lys Leu Ser  
145 150

<210> 2  
<211> 896  
<212> PRT  
<213> Mus musculus

<400> 2

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Ser  
1 5 10 15

Gly Gly Ser Gly Ala Gly Gly Leu Ile Gly Leu Met Lys Asp Ala Phe  
20 25 30

Gln Pro His His His His His Leu Ser Pro His Pro Pro Cys Thr  
35 40 45

Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp Lys Val  
50 55 60

Val Arg Leu Cys Gln Asn Pro Asn Val Ala Leu Lys Asn Ser Pro Pro  
65 70 75 80

Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg Thr Val  
85 90 95

Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn Glu Tyr  
100 105 110

Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln Thr Ile  
115 120 125

Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn Ser Gln  
130 135 140

Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His Met Leu  
145 150 155 160

Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly Asp Thr  
165 170 175

Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys Ala Phe  
180 185 190

Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala Leu His  
195 200 205

Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu Lys Ser  
210 215 220

Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu Phe Asp  
225 230 235 240

Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg Asn Trp  
245 250 255

Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu Thr Tyr  
260 265 270

Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro Gly Ser  
275 280 285

Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala Ile Gly  
290 295 300

Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His Asn Lys  
305 310 315 320

Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe Tyr Leu  
325 330 335

Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu Cys Glu  
340 345 350

Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Ile Cys Ala Glu Asn  
355 360 365

Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met Cys Thr Ser  
370 375 380

Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys Pro Phe Cys  
385 390 395 400

Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp Pro Phe Asp  
405 410 415

Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu Gly Ala Pro  
420 425 430

Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp Asp Ser Leu  
435 440 445

Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg Pro Ser Ser  
450 455 460

Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val Pro Pro Arg  
465 470 475 480

Leu Asp Leu Leu Gln Gln Arg Ala Pro Val Pro Ala Ser Thr Ser Val  
485 490 495

Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His Lys Asp Lys  
500 505 510

Pro Leu Pro Ile Pro Pro Thr Leu Arg Asp Leu Pro Pro Pro Pro Pro  
515 520 525

Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Thr Arg Pro Gln Arg Arg  
530 535 540

Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp Lys Leu Pro  
545 550 555 560

Pro Val Pro Ser Ser Arg Pro Gly Asp Ser Trp Leu Ser Arg Thr Ile  
565 570 575

Pro Lys Val Pro Val Ala Thr Pro Asn Pro Gly Asp Pro Trp Asn Gly  
580 585 590

Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu Pro Ser Gln  
595 600 605

Met Glu Pro Arg Ala Asp Val Pro Arg Leu Gly Ser Thr Phe Ser Leu  
610 615 620

Asp Thr Ser Met Thr Met Asn Ser Ser Pro Val Ala Gly Pro Glu Ser  
625 630 635 640

Glu His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala Ile Tyr Ser  
645 650 655

Leu Ala Ala Arg Pro Leu Pro Met Pro Lys Leu Pro Pro Gly Glu Gln  
660 665 670

Gly Glu Ser Glu Glu Asp Thr Glu Tyr Met Thr Pro Thr Ser Arg Pro  
675 680 685

Val Gly Val Gln Lys Pro Glu Pro Lys Arg Pro Leu Glu Ala Thr Gln  
690 695 700

Ser Ser Arg Ala Cys Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr  
705 710 715 720

Glu Ala Met Tyr Thr Ile Gln Ser Gln Ala Leu Ser Val Ala Glu Asn  
725 730 735

Ser Ala Ser Gly Glu Gly Asn Leu Ala Thr Ala His Thr Ser Thr Gly  
740 745 750

Pro Glu Glu Ser Glu Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro  
755 760 765

Pro Val Pro Ala Val Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn  
770 775 780

Ala Ser Ser Ser Phe Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Asn  
785 790 795 800

Phe Asn Glu Gly Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro  
805 810 815

Arg Arg Ile Asn Ser Glu Arg Lys Ala Ser Ser Tyr Gln Gln Gly Gly  
820 825 830

Gly Ala Thr Ala Asn Pro Val Ala Thr Ala Pro Ser Pro Gln Leu Ser  
835 840 845

Ser Glu Ile Glu Arg Leu Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile  
850 855 860

Gln Lys Ala Leu Val Ile Ala His Asn Asn Ile Glu Met Ala Lys Asn  
865 870 875 880

Ile Leu Arg Glu Phe Val Ser Ile Ser Ser Pro Ala His Val Ala Thr  
885 890 895

<210> 3  
<211> 906  
<212> PRT  
<213> Homo sapiens

<400> 3

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Thr Gly  
1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys

180

185

190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp

420

425

430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala

660

665

670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr

900

905

<210> 4  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 4  
cgtgaagaag agctctgggt t

21

<210> 5  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 5  
gaagatggtg gagaagtgc t

21

<210> 6  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 6  
gatggtgagg aagtgcgtt t

21

<210> 7  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 7  
gtgctggaaag ctcatggact t

21

<210> 8  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 8

gctcatggac aaggtggtgt t

21

<210> 9  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 9  
ggtgtgcgg ttgtgtcagt t

21

<210> 10  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 10  
cccaaagctg gcgctaaagt t

21

<210> 11  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 11  
cccaaagctg gcgctaaagt t

21

<210> 12  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 12  
agctggcgct aaagaatagt t

21

<210> 13  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 13

agaatagccc accttatatt t

21

<210> 14  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 14  
tagccccacct tataatcttat t

21

<210> 15  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 15  
gatatgaggg gaagatggat t

21

<210> 16  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 16  
gatggagaca cttggagaat t

21

<210> 17  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 17  
ctaagcaaac cataaggcctt t

21

<210> 18  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 18

gcaaaccata agcctcttct t

21

<210> 19  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide

<400> 19  
accataagcc tcttcaaggt t

21

<210> 20  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide

<400> 20  
gccttcaa ggagggaaat t

21

<210> 21  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide

<400> 21  
gaaagaatgt atgaggagat t

21

<210> 22  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide

<400> 22  
agaatgtatg aggagaattt t

21

<210> 23  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide

<400> 23

tgtatgagga gaattctcat t

21

<210> 24  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 24  
ttctcagcct aggcgaaact t

21

<210> 25  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 25  
acctaaccaa actgtccctt t

21

<210> 26  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 26  
ccaaactgtc cctcatcttt t

21

<210> 27  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 27  
actgtccctc atcttcagct t

21

<210> 28 .  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 28

ggaatcttc caagtggact t 21

<210> 29  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 29  
tctttccaag tggactcttt t 21

<210> 30  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 30  
gtggactctt tcagggagat t 21

<210> 31  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 31  
agcagatgct gcggaatttt t 21

<210> 32  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 32  
gacaatagtc ctttggaaat t 21

<210> 33  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 33

tagcccttg gaagagcttt t

21

<210> 34  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 34  
gagcttcga caggcttat t

21

<210> 35  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 35  
gtgcatccca tcagttctgt t

21

<210> 36  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 36  
atccactatt gatctgacct t

21

<210> 37  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 37  
tttgacatct ttacccgact t

21

<210> 38  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 38

ttggaacagc cttgctgtat t

21

<210> 39  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 39  
cagccttgct gtaactcatt t

21

<210> 40  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 40  
ctcatcctgg ctacatggct t

21

<210> 41  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 41  
gtgaaagctc ggctccagat t

21

<210> 42  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 42  
agctcggctc cagaaattct t

21

<210> 43  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 43

attcattcac aaacctggct t

21

<210> 44  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 44  
acctggcagt tataatcttct t

21

<210> 45  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 45  
cattctccag acaatccctt t

21

<210> 46  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 46  
tccctcacaa taaaaccttt t

21

<210> 47  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 47  
taaacctctc ttccaagcat t

21

<210> 48  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 48

acctctcttc caagcactgt t

21

<210> 49  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 49  
gcactgattg atggcttcatt t

21

<210> 50  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 50  
ggcttctatt tgtttcctgt t

21

<210> 51  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 51  
atcagaatcc tgcgtact t

21

<210> 52  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 52  
tcctgatctg actggcttat t

21

<210> 53  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 53

ccaactcccc aagaccatat t

21

<210> 54  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 54  
ctccccaaga ccatatcaat t

21

<210> 55  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 55  
gaccatatca aagtgaccct t

21

<210> 56  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 56  
agtgaccctt gaacaatatt t

21

<210> 57  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 57  
caatatgaat tatactgtgt t

21

<210> 58  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 58

tatgaattat actgtgagat t

21

<210> 59  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 59  
ttatactgtg agatgggctt t

21

<210> 60  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 60  
tgataaggat gtaaaagattt t

21

<210> 61  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 61  
ggatgtaaag attgagccct t

21

<210> 62  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 62  
agattgagcc ctgtggacat t

21

<210> 63  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 63

tcagaaggtc agggctgtct t

21

<210> 64  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 64  
ggtcagggct gtcctttctt t

21

<210> 65  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 65  
attaaaggtt ctgaacccat t

21

<210> 66  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 66  
aggtactgaa cccatcggt t

21

<210> 67  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 67  
cccatcggtt tagatccgtt t

21

<210> 68  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 68

attatgatga tcatgtatgtat t

21

<210> 69  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 69  
cgagctgatg atactctctt t

21

<210> 70  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 70  
ggaattggct ggtgccaaagt t

21

<210> 71  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 71  
ttggctggtg ccaaggtgg t

21

<210> 72  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 72  
cggccgcctt ctccattctt t

21

<210> 73  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 73

gtgcttctgc tcttggaaact t

21

<210> 74  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 74  
ctgcttctaa ggctgcttct t

21

<210> 75  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 75  
ggctgcttct ggctcccttt t

21

<210> 76  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 76  
agacaaacca ttgccagttat t

21

<210> 77  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 77  
accattgccca gtacctccct t

21

<210> 78  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 78

tcccgacctc aaagacgcct t

21

<210> 79  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 79  
agacgccccct tgccttgtat t

21

<210> 80  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 80  
tccccaaagt accagtatct t

21

<210> 81  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 81  
agtaccagta tctgccccat t

21

<210> 82  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 82  
gttccagtga tccctggact t

21

<210> 83  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 83

gagaat~~taac~~ caaccggcat t

21

<210> 84  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide

<400> 84  
ttaacc~~aa~~acc ggcactcact t

21

<210> 85  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide

<400> 85  
ccaaccggca ctcacttcct t

21

<210> 86  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide

<400> 86  
ccggca~~ct~~actca cttccat~~ttt~~ t

21

<210> 87  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide

<400> 87  
atggagccca gaccagatgt t

21

<210> 88  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide

<400> 88

gcacgttcag tctggatact t 21

<210> 89  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 89  
tagcagccca ttagtaggtt t 21

<210> 90  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 90  
tcaaaccttc ctcatctgct t 21

<210> 91  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 91  
actttcctca tctgccaatt t 21

<210> 92  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 92  
tgccatttat tctctggctt t 21

<210> 93  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 93

ctgccacctg gggagcaatt t 21

<210> 94  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 94  
tgtgagggtg aagaggacat t 21

<210> 95  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 95  
gaggacacag agtacatgat t 21

<210> 96  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 96  
gcaatgtata atattcagtt t 21

<210> 97  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 97  
tgtataataat tcagtcccat t 21

<210> 98  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 98

tattcagtcc caggcgccat t

21

<210> 99  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 99  
cactggtccc gaggagtcat t

21

<210> 100  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 100  
tgaggatgat gggtatgatt t

21

<210> 101  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 101  
ctctctcaga tatctctaatt t

21

<210> 102  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 102  
tgccagctcc tccttggct t

21

<210> 103  
<211> 21  
<212> DNA  
<213> artificial  
  
<220>  
<223> siRNA sense strand oligonucleotide  
  
<400> 103

caaatgtcac tgaaggttct t

21

<210> 104  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 104  
atgtcaactga aggttcccat t

21

<210> 105  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 105  
ggttcccaag ttcccgagat t

21

<210> 106  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 106  
gttcccgaga ggcctccaat t

21

<210> 107  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 107  
ccattcccgc ggagaatcat t

21

<210> 108  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 108

tcaactctga acggaaagct t 21

<210> 109  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 109  
ctctgaacgg aaagctggct t 21

<210> 110  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 110  
cggaaagctg gcagctgtct t 21

<210> 111  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 111  
agctggcagc tgtcagcaat t 21

<210> 112  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 112  
cctcatgagt caggggtact t 21

<210> 113  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 113

agctttggtc attgccagg t 21

<210> 114  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 114  
caacatcgag atggccaaat t 21

<210> 115  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 115  
acatcctccg ggaatttgtt t 21

<210> 116  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 116  
tttggttcca tttcttctct t 21

<210> 117  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 117  
gtggcaccta gaagggcagt t 21

<210> 118  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 118

gggcaggagt tccttggtt t

21

<210> 119  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 119  
gtcttgccct ctctgtgggt t

21

<210> 120  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 120  
gatttcaaag tggtaaaatt t

21

<210> 121  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA sense strand oligonucleotide

<400> 121  
tggagcagct agtatgtttt t

21

<210> 122  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 122  
cccagagctc ttcttcacgt t

21

<210> 123  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 123

gcacttctcc accatcttct t

21

<210> 124  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 124  
ccagcaactc tccaccatct t

21

<210> 125  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 125  
gtccatgagc ttccagcact t

21

<210> 126  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 126  
caccacccgt tccatgagct t

21

<210> 127  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 127  
ctgacacacaac cgcaccacct t

21

<210> 128  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 128

cttttagcgcc agctttgggt t

21

<210> 129  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 129  
cttttagcgcc agctttgggt t

21

<210> 130  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 130  
ctattcttta gcgccagctt t

21

<210> 131  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 131  
atataaggtg ggctattctt t

21

<210> 132  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 132  
taagatataa ggtgggctat t

21

<210> 133  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 133

tccatcttcc cctcatatct t

21

<210> 134  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 134  
ttctccaagt gtctccatct t

21

<210> 135  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 135  
aggcttatgg tttgcttagt t

21

<210> 136  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 136  
gaagaggctt atggtttgct t

21

<210> 137  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 137  
ccttgaagag gcttatggtt t

21

<210> 138  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 138

tttccctcct tgaagaggct t

21

<210> 139  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 139  
tctcctcata cattctttct t

21

<210> 140  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 140  
aattctcctc atacattctt t

21

<210> 141  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 141  
tgagaattct cctcatacat t

21

<210> 142  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 142  
gtttcgcccta ggctgagaat t

21

<210> 143  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 143

agggacagtt tggtaggtt t

21

<210> 144  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 144  
aagatgaggg acagtttgggt t

21

<210> 145  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 145  
gctgaagatg agggacagtt t

21

<210> 146  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 146  
gtccacttgg aaagattcct t

21

<210> 147  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 147  
aagagtccac ttggaaagat t

21

<210> 148  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 148

tctccctgaa agagtccact t

21

<210> 149  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 149  
aaattccgca gcatctgctt t

21

<210> 150  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 150  
cttccaaggg actattgtct t

21

<210> 151  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 151  
aagctcttcc aaggactat t

21

<210> 152  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 152  
tagagcctgt cgaaaagctct t

21

<210> 153  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 153

cagaactgat gggatgcact t

21

<210> 154  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 154  
ggtcagatca atagtggatt t

21

<210> 155  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 155  
gtcgggtaaa gatgtcaaat t

21

<210> 156  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 156  
tacagcaagg ctgttccaat t

21

<210> 157  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 157  
atgagttaca gcaaggctgt t

21

<210> 158  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 158

gccatgtgc caggatgagt t

21

<210> 159  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 159  
tctggagccg agctttcact t

21

<210> 160  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 160  
gaatttctgg agccgagctt t

21

<210> 161  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 161  
gccagggttg tgaatgaatt t

21

<210> 162  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 162  
gaagatataaa ctgccaggtt t

21

<210> 163  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 163

agggattgtc tggagaatgt t 21

<210> 164  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 164  
agaggtttat tgtgagggat t 21

<210> 165  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 165  
tgcttggaaag agaggtttat t 21

<210> 166  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 166  
cagtgcgtgg aagagaggat t 21

<210> 167  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 167  
tgaagccatc aatcagtgt t 21

<210> 168  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 168

cagggaaacaa atagaaggct t

21

<210> 169  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 169  
gtcagatcag gattctgatt t

21

<210> 170  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 170  
taagccagtc agatcaggat t

21

<210> 171  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 171  
tatggtcttg gggagttgg t

21

<210> 172  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 172  
ttgatatgg tttggggagt t

21

<210> 173  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 173

gggtcacttt gatatggtct t

21

<210> 174  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 174  
atattgttcc tgggtcactt t

21

<210> 175  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 175  
cacagtataa ttcatattgt t

21

<210> 176  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 176  
tctcacagta taattcatat t

21

<210> 177  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 177  
agcccatctc acagtataat t

21

<210> 178  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 178

aatcttaca tccttatcat t

21

<210> 179  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 179  
gggctcaatc tttacatcct t

21

<210> 180  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 180  
tgtccacagg gctcaatctt t

21

<210> 181  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 181  
gacagccctg accttctgat t

21

<210> 182  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 182  
agaaaggaca gccctgaccc t

21

<210> 183  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 183

tgggttcagt acctttaatt t

21

<210> 184  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 184  
cacgatgggt tcagtagctt t

21

<210> 185  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 185  
acggatctac cacgatgggt t

21

<210> 186  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 186  
tcatcatcat catcataatt t

21

<210> 187  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 187  
agagagtatc atcagtcgt t

21

<210> 188  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 188

cttggcacca gccaaattcct t

21

<210> 189  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 189  
ccaccttggc accagccaa t

21

<210> 190  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 190  
agaatggaga aggcgccgt t

21

<210> 191  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 191  
gttccaagag cagaagcact t

21

<210> 192  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 192  
gaagcagcct tagaaggcgt t

21

<210> 193  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 193

aagggagcca gaagcagcct t

21

<210> 194  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 194  
tactggcaat ggtttgtctt t

21

<210> 195  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 195  
gggaggtact ggcaatgggt t

21

<210> 196  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 196  
ggcgtcttg aggtcgggt t

21

<210> 197  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 197  
tacaaggcaa gggcgtctt t

21

<210> 198  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 198

gatactggta ctttggggat t

21

<210> 199  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 199  
tggggcagat actggtaatt t

21

<210> 200  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 200  
gtccaggat cactggaact t

21

<210> 201  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 201  
tgcccggttgg ttaattctct t

21

<210> 202  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 202  
tgagtgccg gttggtaat t

21

<210> 203  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 203

ggaagtgagt gccgggtggg t 21

<210> 204  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 204  
aatggaaagt gagtgccgg t 21

<210> 205  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 205  
catctggtct gggctccatt t 21

<210> 206  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 206  
gtatccagac tgaacgtgct t 21

<210> 207  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 207  
acctactaat gggctgctat t 21

<210> 208  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 208

gcagatgagg aaggtttcat t

21

<210> 209  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 209  
attggcagat gaggaaggtt t

21

<210> 210  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 210  
agccagagaa taaatggcat t

21

<210> 211  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 211  
attgctcccc aggtggcagt t

21

<210> 212  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 212  
tgtcctcttc accctcacat t

21

<210> 213  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 213

tcatgtactc tggtcctct t

21

<210> 214  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 214  
actgaatatt atacattgct t

21

<210> 215  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 215  
tgggactgaa tattatacat t

21

<210> 216  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 216  
tggcgccctgg gactgaatat t

21

<210> 217  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 217  
tgactcctcg ggaccagtgt t

21

<210> 218  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 218

atcataacca tcatcctcat t

21

<210> 219  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 219  
ttagagatat ctgagagagt t

21

<210> 220  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 220  
gccaaaggag gagctggcat t

21

<210> 221  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 221  
gaaccttcag tgacatttgt t

21

<210> 222  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 222  
tggaaacctt cagtgacatt t

21

<210> 223  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 223

tctcggaac ttgggaacct t

21

<210> 224  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 224  
ttggaggcct ctcgggaact t

21

<210> 225  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 225  
tgattctccg cgggaatgg t

21

<210> 226  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 226  
gcttccgtt cagagttgat t

21

<210> 227  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 227  
gccagcttc cgttcagagt t

21

<210> 228  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 228

gacagctgcc agctttccgt t

21

<210> 229  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 229  
ttgctgacag ctgccagctt t

21

<210> 230  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 230  
gtaccctcta ctcatgagg t

21

<210> 231  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 231  
ctggcaatg accaaagctt t

21

<210> 232  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 232  
tttggccatc tcgatgtt t

21

<210> 233  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 233

acaaattccc ggaggatgtt t

21

<210> 234  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 234  
gagaagaaat ggaaacaaat t

21

<210> 235  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 235  
ctgcccttct aggtgccact t

21

<210> 236  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 236  
accaaaggaa ctcctgccct t

21

<210> 237  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 237  
cccacagaga gggcaagact t

21

<210> 238  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 238

atttcaccac tttgaaatct t

21

<210> 239  
<211> 21  
<212> DNA  
<213> artificial

<220>  
<223> siRNA antisense strand oligonucleotide

<400> 239  
aaacatacta gctgctccat t

21

<210> 240  
<211> 3  
<212> DNA  
<213> artificial

<220>  
<223> shRNA loop sequence

<400> 240  
ccc

3

<210> 241  
<211> 4  
<212> DNA  
<213> artificial

<220>  
<223> shRNA loop sequence

<400> 241  
ttcg

4

<210> 242  
<211> 5  
<212> DNA  
<213> artificial

<220>  
<223> shRNA loop sequence

<400> 242  
ccacc

5

<210> 243  
<211> 6  
<212> DNA  
<213> artificial

<220>  
<223> shRNA loop sequence

<400> 243

ctcgag

6

<210> 244  
<211> 6  
<212> DNA  
<213> artificial  
  
<220>  
<223> shRNA loop sequence  
  
<400> 244  
aagctt

6

<210> 245  
<211> 7  
<212> DNA  
<213> artificial  
  
<220>  
<223> shRNA loop sequence  
  
<400> 245  
ccacacc

7

<210> 246  
<211> 9  
<212> DNA  
<213> artificial  
  
<220>  
<223> shRNA loop sequence  
  
<400> 246  
ttcaagaga

9

<210> 247  
<211> 2721  
<212> DNA  
<213> artificial  
  
<220>  
<223> c-Cbl G306E mutant  
  
<220>  
<221> CDS  
<222> (1)..(2718)

<400> 247  
atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc acg ggc  
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

48

tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc  
Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

96

ttc cag ccg cac cac cac cac cac ctc agc ccc cac ccg ccg	35	40	45	144
Phe Gln Pro His				
Leu Ser Pro His Pro Pro				
50	55	60		192
ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac				
Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp				
65	70	75	80	240
aag gtg gtg cgg ttg tgt cag aac cca aag ctg gcg cta aag aat agc				
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser				
85	90	95		288
cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt				
Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg				
100	105	110		336
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat				
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn				
115	120	125		384
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa				
Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln				
130	135	140		432
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac				
Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His				
145	150	155	160	480
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga				
Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly				
165	170	175		528
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa				
Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys				
180	185	190		576
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct				
Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala				
195	200	205		624
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg				
Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu				
210	215	220		672
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa				
Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu				
225	230	235	240	720
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg				
Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg				
245	250	255		768
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg				
Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu				
260	265	270		816

acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct	864
Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro	
275 280 285	
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct	912
Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala	
290 295 300	
att gag tat gtt act gct gat ggg aac att ctc cag aca atc cct cac	960
Ile Glu Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His	
305 310 315 320	
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc	1008
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe	
325 330 335	
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta	1056
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu	
340 345 350	
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat	1104
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr	
355 360 365	
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt	1152
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys	
370 375 380	
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg	1200
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met	
385 390 395 400	
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt	1248
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys	
405 410 415	
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat	1296
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp	
420 425 430	
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag	1344
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu	
435 440 445	
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat	1392
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp	
450 455 460	
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg	1440
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg	
465 470 475 480	
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg	1488
Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val	
485 490 495	
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt	1536
Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser	
500 505 510	

gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515 520 525	1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530 535 540	1632
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545 550 555 560	1680
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565 570 575	1728
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580 585 590	1776
cgg cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595 600 605	1824
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610 615 620	1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625 630 635 640	1920
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645 650 655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala 660 665 670	2016
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675 680 685	2064
ggg gag caa tgt gag ggt gaa gag gac aca gag tac atg act ccc tct Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser 690 695 700	2112
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys 705 710 715 720	2160
gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn 725 730 735	2208
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu 740 745 750	2256

ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu 755 760 765	2304
aat gag gat gat ggg tat gat gtc cca aag cca cct gtg ccg gcc gtg Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val 770 775 780	2352
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe 785 790 795 800	2400
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly 805 810 815	2448
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg ccg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820 825 830	2496
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala 835 840 845	2544
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu 850 855 860	2592
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile 865 870 875 880	2640
gcc cag aac aac atc gag atg gcc aaa aac atc ctc ccg gaa ttt gtt Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val 885 890 895	2688
tcc att tct tct cct gcc cat gta gct acc tag Ser Ile Ser Ser Pro Ala His Val Ala Thr 900 905	2721

<210> 248  
 <211> 906  
 <212> PRT  
 <213> artificial  
  
 <220>  
 <223> Synthetic Construct  
  
 <400> 248

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
 1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala  
 20 25 30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220.

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Glu Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 249  
<211> 2721  
<212> DNA  
<213> artificial

<220>  
<223> c-Cbl C381A mutant

<220>  
<221> CDS  
<222> (1)...(2718)

<400> 249  
atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc 48  
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc 96  
Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala

20

25

30

ttc cag ccg cac cac cac cac cac cac ctc agc ccc cac ccg ccg	35	40	45	144
Phe Gln Pro His				
50	55	60		192
ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac				
Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp				
65	70	75	80	240
aag gtg gtg cggttg cag aac cca aag ctg gcg cta aag aat agc				
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser				
100	105	110		288
cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt				
Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg				
130	135	140	95	
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat				
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn				
165	170	175	180	336
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa				
Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln				
195	200	205	210	384
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat				
Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn				
225	230	235	240	432
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac				
Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His				
255	260	265	270	480
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga				
Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly				
295	300	305	310	528
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa				
Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys				
330	335	340	345	576
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct				
Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala				
365	370	375	380	624
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg				
Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu				
405	410	415	420	672
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa				
Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu				
435	440	445	450	720
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg				
Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg				
475	480	485	490	768
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg				
Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu				
515	520	525	530	816

260	265	270	
acg tat gac gaa gtg aaa gct cg <sup>g</sup> ctc cag aaa ttc att cac aaa cct Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro	275	280	864
285			
ggc agt tat atc ttc cg <sup>g</sup> ctg agc tgt act cgt ctg ggt cag tgg gct Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala	290	295	912
300			
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His	305	310	960
315		320	
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe	325	330	1008
335			
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu	340	345	1056
350			
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr	355	360	1104
365			
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta gct aaa ata tgt Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Ala Lys Ile Cys	370	375	1152
380			
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met	385	390	1200
395		400	
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys	405	410	1248
415			
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp	420	425	1296
430			
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu	435	440	1344
445			
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp	450	455	1392
460			
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cg <sup>g</sup> Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg	465	470	1440
475		480	
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val	485	490	1488
495			
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser			1536

500	505	510	
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515	520	525	1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530	535	540	1632
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545	550	555	1680
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565	570	575	1728
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580	585	590	1776
cgg cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595	600	605	1824
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610	615	620	1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625	630	635	1920
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Asn Ser Ser Pro Leu Val Gly 645	650	655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ala Asn Ala 660	665	670	2016
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675	680	685	2064
ggg gag caa tgt gag ggt gaa gag gac aca gag tac atg act ccc tct Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser 690	695	700	2112
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys 705	710	715	2160
gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn 725	730	735	2208
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu			2256

740	745	750	
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa			2304
Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu			
755	760	765	
aat gag gat gat ggg tat gat gtc cca aag cca cct gtg ccg gcc gtg			2352
Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val			
770	775	780	
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt			2400
Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe			
785	790	795	800
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt			2448
Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly			
805	810	815	
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg ccg aga atc aac			2496
Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn			
820	825	830	
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc			2544
Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala			
835	840	845	
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc			2592
Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu			
850	855	860	
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att			2640
Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile			
865	870	875	880
gcc cag aac aac atc gag atg gcc aaa aac atc ctc ccg gaa ttt gtt			2688
Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val			
885	890	895	
tcc att tct tct cct gcc cat gta gct acc tag			2721
Ser Ile Ser Ser Pro Ala His Val Ala Thr			
900	905		

<210> 250  
 <211> 906  
 <212> PRT  
 <213> artificial

<220>  
 <223> Synthetic Construct

<400> 250

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Thr Gly  
 1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
 20 25 30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Ala Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525.

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 251  
<211> 2721  
<212> DNA  
<213> artificial

<220>  
<223> c-Cbl Y700F mutant

<220>  
<221> CDS  
<222> (1)..(2718)

<400> 251  
atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc 48  
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gcc 96

Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Leu	Ile	Gly	Leu	Met	Lys	Asp	Ala	
20					25							30				
ttc	cag	ccg	cac	cac	cac	cac	cac	ctc	agc	ccc	cac	ccg	ccg			144
Phe	Gln	Pro	His	His	His	His	His	His	Leu	Ser	Pro	His	Pro	Pro		
35					40							45				
ggg	acg	gtg	gac	aag	aag	atg	gtg	gag	aag	tgc	tgg	aag	ctc	atg	gac	
Gly	Thr	Val	Asp	Lys	Lys	Met	Val	Glu	Lys	Cys	Trp	Lys	Leu	Met	Asp	
50				55							60					192
aag	gtg	gtg	cg	ttg	tgt	cag	aac	cca	aag	ctg	g	ct	aag	aat	agc	
Lys	Val	Val	Arg	Leu	Cys	Gln	Asn	Pro	Lys	Leu	Ala	Leu	Lys	Asn	Ser	
65				70				85		75			80			240
cca	cct	tat	atc	tta	gac	ctg	cta	cca	gat	acc	ta	cag	cat	ctc	cgt	
Pro	Pro	Tyr	Ile	Leu	Asp	Leu	Leu	Pro	Asp	Thr	Tyr	Gln	His	Leu	Arg	
85				90							95					288
act	atc	ttg	tca	aga	tat	gag	ggg	aag	atg	gag	aca	ctt	gga	gaa	aat	
Thr	Ile	Leu	Ser	Arg	Tyr	Glu	Gly	Lys	Met	Glu	Thr	Leu	Gly	Glu	Asn	
100				105							110					336
gag	tat	ttt	agg	gtg	ttt	atg	gag	aat	ttg	atg	aag	aaa	act	aag	caa	
Glu	Tyr	Phe	Arg	Val	Phe	Met	Glu	Asn	Leu	Met	Lys	Lys	Thr	Lys	Gln	
115				120							125					384
acc	ata	agc	ctc	ttc	aag	gag	gga	aaa	gaa	aga	atg	tat	gag	gag	aat	
Thr	Ile	Ser	Leu	Phe	Lys	Glu	Gly	Lys	Glu	Arg	Met	Tyr	Glu	Glu	Asn	
130				135					140							432
tct	cag	cct	agg	cga	aac	cta	acc	aaa	ctg	tcc	ctc	atc	ttc	agc	cac	
Ser	Gln	Pro	Arg	Arg	Asn	Leu	Thr	Lys	Leu	Ser	Leu	Ile	Phe	Ser	His	
145				150					155			160				480
atg	ctg	gca	gaa	cta	aaa	gga	atc	ttt	cca	agt	gga	ctc	ttt	cag	gga	
Met	Leu	Ala	Glu	Leu	Lys	Gly	Ile	Phe	Pro	Ser	Gly	Leu	Phe	Gln	Gly	
165				170							175					528
gac	aca	ttt	cg	att	act	aaa	gca	gat	gct	g	gaa	ttt	tgg	aga	aaa	
Asp	Thr	Phe	Arg	Ile	Thr	Lys	Ala	Asp	Ala	Ala	Glu	Phe	Trp	Arg	Lys	
180				185							190					576
gct	ttt	ggg	gaa	aag	aca	ata	gtc	cct	tgg	aag	agc	ttt	cga	cag	gct	
Ala	Phe	Gly	Glu	Lys	Thr	Ile	Val	Pro	Trp	Lys	Ser	Phe	Arg	Gln	Ala	
195				200					205							624
cta	cat	gaa	gt	cat	ccc	atc	agt	tct	gg	ctg	gag	gg	at	gt	ct	
Leu	His	Glu	Val	His	Pro	Ile	Ser	Ser	Gly	Leu	Glu	Ala	Met	Ala	Leu	
210				215					220							672
aaa	tcc	act	att	gat	ctg	acc	tgc	aat	gat	tat	att	tcg	gtt	ttt	gaa	
Lys	Ser	Thr	Ile	Asp	Leu	Thr	Cys	Asn	Asp	Tyr	Ile	Ser	Val	Phe	Glu	
225				230					235			240				720
ttt	gac	atc	ttt	acc	cga	ctc	ttt	cag	ccc	tgg	tcc	tct	ttg	ctc	agg	
Phe	Asp	Ile	Phe	Thr	Arg	Leu	Phe	Gln	Pro	Trp	Ser	Ser	Leu	Leu	Arg	
245				250							255					768
aat	tgg	aac	agc	ctt	gct	gta	act	cat	cct	ggc	tac	atg	gct	ttt	ttg	
																816

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu			
260	265	270	
acg tat gac gaa gtc aaa gct cgg ctc cag aaa ttc att cac aaa cct			864
Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro			
275	280	285	
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct			912
Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala			
290	295	300	
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac			960
Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His			
305	310	315	320
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc			1008
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe			
325	330	335	
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta			1056
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu			
340	345	350	
tgt gaa cca act ccc caa gac cat atc aaa gtc acc cag gaa caa tat			1104
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr			
355	360	365	
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt			1152
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys			
370	375	380	
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg			1200
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met			
385	390	395	400
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt			1248
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys			
405	410	415	
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtc gta gat			1296
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp			
420	425	430	
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag			1344
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu			
435	440	445	
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat			1392
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp			
450	455	460	
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtc gaa cgg			1440
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg			
465	470	475	480
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg			1488
Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val			
485	490	495	
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt			1536

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser			
500	505	510	
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat			1584
Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His			
515	520	525	
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca			1632
Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro			
530	535	540	
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct			1680
Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro			
545	550	555	560
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac			1728
Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp			
565	570	575	
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc			1776
Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro			
580	585	590	
cgg cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc			1824
Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Asp Pro			
595	600	605	
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg			1872
Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu			
610	615	620	
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg			1920
Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr			
625	630	635	640
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt			1968
Phe Ser Leu Asp Thr Ser Met Ser Asn Ser Ser Pro Leu Val Gly			
645	650	655	
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc			2016
Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala			
660	665	670	
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct			2064
Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro			
675	680	685	
ggg gag caa tgt gag ggt gaa gag gac aca gag ttc atg act ccc tct			2112
Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Phe Met Thr Pro Ser			
690	695	700	
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt			2160
Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys			
705	710	715	720
gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat			2208
Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn			
725	730	735	
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa			2256

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu		
740	745	750
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa		2304
Gly Asn Leu Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu		
755	760	765
aat gag gat gat ggg tat gat gtc cca aag cca cct gtg ccg gcc gtg		2352
Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val		
770	775	780
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt		2400
Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe		
785	790	795
800		
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt		2448
Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly		
805	810	815
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg cgg aga atc aac		2496
Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn		
820	825	830
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc		2544
Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala		
835	840	845
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc		2592
Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu		
850	855	860
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att		2640
Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile		
865	870	875
880		
gcc cag aac aac atc gag atg gcc aaa aac atc ctc ccg gaa ttt gtt		2688
Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val		
885	890	895
tcc att tct tct cct gcc cat gta gct acc tag		2721
Ser Ile Ser Ser Pro Ala His Val Ala Thr		
900	905	

<210> 252  
 <211> 906  
 <212> PRT  
 <213> artificial

<220>  
 <223> Synthetic Construct

<400> 252

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
 1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
 20 25 30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro  
 35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
 100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
 115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn	Trp	Asn	Ser	Leu	Ala	Val	Thr	His	Pro	Gly	Tyr	Met	Ala	Phe	Leu
260							265						270		

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Phe Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 253  
<211> 2721  
<212> DNA  
<213> artificial

<220>  
<223> c-Cbl Y731F mutant

<220>  
<221> CDS  
<222> (1)..(2718)

<400> 253  
atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc  
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

48

tcc	ggg	ggc	tcg	ggt	tcg	ggt	ggc	ctg	att	ggg	ctc	atg	aag	gac	gcc	96
Ser	Gly	Gly	Ser	Gly	Ser	Gly	Gly	Leu	Ile	Gly	Leu	Met	Lys	Asp	Ala	
20			25			30										
ttc	cag	ccg	cac	cac	cac	cac	cac	ctc	agc	ccc	cac	ccg	ccg		144	
Phe	Gln	Pro	His	His	His	His	His	His	Leu	Ser	Pro	His	Pro	Pro		
35			40			45										
ggg	acg	gtg	gac	aag	aag	atg	gtg	gag	aag	tgc	tgg	aag	ctc	atg	gac	192
Gly	Thr	Val	Asp	Lys	Lys	Met	Val	Glu	Lys	Cys	Trp	Lys	Leu	Met	Asp	
50			55			60										
aag	gtg	gtg	cg	ttg	tgt	cag	aac	cca	aag	ctg	g	ct	aag	aat	agc	240
Lys	Val	Val	Arg	Leu	Cys	Gln	Asn	Pro	Lys	Leu	Ala	Leu	Lys	Asn	Ser	
65			70			75										
cca	cct	tat	atc	tta	gac	ctg	cta	cca	gat	acc	ta	cag	cat	ctc	cgt	288
Pro	Pro	Tyr	Ile	Leu	Asp	Leu	Leu	Pro	Asp	Thr	Tyr	Gln	His	Leu	Arg	
85			90			95										
act	atc	ttg	tca	aga	tat	gag	ggg	aag	atg	gag	aca	ctt	gga	gaa	aat	336
Thr	Ile	Leu	Ser	Arg	Tyr	Glu	Gly	Lys	Met	Glu	Thr	Leu	Gly	Glu	Asn	
100			105			110										
gag	tat	ttt	agg	gtg	ttt	atg	gag	aat	ttg	atg	aag	aaa	act	aag	caa	384
Glu	Tyr	Phe	Arg	Val	Phe	Met	Glu	Asn	Leu	Met	Lys	Lys	Thr	Lys	Gln	
115			120			125										
acc	ata	agc	ctc	tcc	aag	gag	gga	aaa	gaa	aga	atg	tat	gag	gag	aat	432
Thr	Ile	Ser	Leu	Phe	Lys	Glu	Gly	Lys	Glu	Arg	Met	Tyr	Glu	Glu	Asn	
130			135			140										
tct	cag	cct	agg	cga	aac	cta	acc	aaa	ctg	tcc	ctc	atc	tcc	agc	cac	480
Ser	Gln	Pro	Arg	Arg	Asn	Leu	Thr	Lys	Leu	Ser	Leu	Ile	Phe	Ser	His	
145			150			155										
atg	ctg	gca	gaa	cta	aaa	gga	atc	ttt	cca	agt	gga	ctc	ttt	cag	gga	528
Met	Leu	Ala	Glu	Leu	Lys	Gly	Ile	Phe	Pro	Ser	Gly	Leu	Phe	Gln	Gly	
165			170			175										
gac	aca	ttt	cgg	att	act	aaa	gca	gat	gct	g	ca	tgg	aga	aaa	576	
Asp	Thr	Phe	Arg	Ile	Thr	Lys	Ala	Asp	Ala	Ala	Glu	Phe	Trp	Arg	Lys	
180			185			190										
gct	ttt	ggg	gaa	aag	aca	ata	gtc	cct	tgg	aag	agc	ttt	cga	cag	gct	624
Ala	Phe	Glu	Lys	Thr	Ile	Val	Pro	Trp	Lys	Ser	Phe	Arg	Gln	Ala		
195			200			205										
cta	cat	gaa	gtg	cat	ccc	atc	agt	tct	ggg	ctg	gag	gcc	atg	gct	ctg	672
Leu	His	Glu	Val	His	Pro	Ile	Ser	Ser	Gly	Leu	Glu	Ala	Met	Ala	Leu	
210			215			220										
aaa	tcc	act	att	gat	ctg	acc	tgc	aat	gat	tat	att	tcg	gtt	ttt	gaa	720
Lys	Ser	Thr	Ile	Asp	Leu	Thr	Cys	Asn	Asp	Tyr	Ile	Ser	Val	Phe	Glu	
225			230			235										
ttt	gac	atc	ttt	acc	cga	ctc	ttt	cag	ccc	tgg	tcc	tct	ttg	ctc	agg	768
Phe	Asp	Ile	Phe	Thr	Arg	Leu	Phe	Gln	Pro	Trp	Ser	Ser	Leu	Leu	Arg	
245			250			255										

aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu 260 265 270	816
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro 275 280 285	864
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala 290 295 300	912
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His 305 310 315 320	960
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe 325 330 335	1008
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu 340 345 350	1056
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr 355 360 365	1104
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys 370 375 380	1152
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met 385 390 395 400	1200
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys 405 410 415	1248
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp 420 425 430	1296
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu 435 440 445	1344
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp 450 455 460	1392
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg 465 470 475 480	1440
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val 485 490 495	1488

cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser 500 505 510	1536
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515 520 525	1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530 535 540	1632
cca ccg cct cca gac ccg cca tat tct gtt gga gca gaa tcc cga cct Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545 550 555 560	1680
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565 570 575	1728
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580 585 590	1776
cg <sup>g</sup> cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595 600 605	1824
tgg aca gga aga gaa tta acc aac cg <sup>g</sup> cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610 615 620	1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625 630 635 640	1920
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645 650 655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala 660 665 670	2016
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675 680 685	2064
ggg gag caa tgt gag ggt gaa gag gac aca gag tac atg act ccc tct Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser 690 695 700	2112
tcc agg cct cta cg <sup>g</sup> cct ttg gat aca tcc cag agt tca cga gca tgt Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys 705 710 715 720	2160
gat tgc gac cag cag att gat agc tgt acg ttt gaa gca atg tat aat Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Phe Glu Ala Met Tyr Asn 725 730 735	2208

att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu 740 745 750	2256
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa Gly Asn Leu Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu 755 760 765	2304
aat gag gat gat ggg tat gat gtc cca aag cca cct gtg ccg gcc gtg Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val 770 775 780	2352
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe 785 790 795 800	2400
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly 805 810 815	2448
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg ccg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820 825 830	2496
tct gaa cg <sup>g</sup> aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala 835 840 845	2544
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu 850 855 860	2592
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile 865 870 875 880	2640
gcc cag aac aac atc gag atg gcc aaa aac atc ctc ccg gaa ttt gtt Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val 885 890 895	2688
tcc att tct cct gcc cat gta gct acc tag Ser Ile Ser Ser Pro Ala His Val Ala Thr 900 905	2721

<210> 254  
<211> 906  
<212> PRT  
<213> artificial

<220>  
<223> Synthetic Construct

<400> 254

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala

20

25

30

Phe Gln Pro His His His His His His His Leu Ser Pro His Pro Pro  
 35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
 50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
 65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
 85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
 100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
 115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
 130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
 145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
 165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
 180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
 195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
 210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
 225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
 245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu

260

265

270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser

500

505

510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Asp Thr Glu Tyr Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Phe Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu

740

745

750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Tyr Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 255  
<211> 2721  
<212> DNA  
<213> artificial

<220>  
<223> c-Cbl Y774F mutant

<220>  
<221> CDS  
<222> (1)..(2718)

<400> 255  
atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc  
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
1 5 10 15

48

tcc	ggg	ggc	tcg	ggt	tcg	ggt	ggc	ctg	att	ggg	ctc	atg	aag	gac	gcc	96
Ser	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Gly	Leu	Ile	Gly	Leu	Met	Lys	Asp	Ala
20									25							30
ttc	cag	ccg	cac	cac	cac	cac	cac	cac	ctc	agc	ccc	cac	ccg	ccg	144	
Phe	Gln	Pro	His	Leu	Ser	Pro	His	Pro	Pro							
35									40							45
ggg	acg	gtg	gac	aag	aag	atg	gtg	gag	aag	tgc	tgg	aag	ctc	atg	gac	192
Gly	Thr	Val	Asp	Lys	Lys	Met	Val	Glu	Lys	Cys	Trp	Lys	Leu	Met	Asp	
50							55					60				
aag	gtg	gtg	cgg	ttg	tgt	cag	aac	cca	aag	ctg	gcg	cta	aag	aat	agc	240
Lys	Val	Val	Arg	Leu	Cys	Gln	Asn	Pro	Lys	Leu	Ala	Leu	Lys	Asn	Ser	
65							70			75			80			
cca	cct	tat	atc	tta	gac	ctg	cta	cca	gat	acc	tac	cag	cat	ctc	cgt	288
Pro	Pro	Tyr	Ile	Leu	Asp	Leu	Leu	Pro	Asp	Thr	Tyr	Gln	His	Leu	Arg	
							85			90			95			
act	atc	ttg	tca	aga	tat	gag	ggg	aag	atg	gag	aca	ctt	gga	gaa	aat	336
Thr	Ile	Leu	Ser	Arg	Tyr	Glu	Gly	Lys	Met	Glu	Thr	Leu	Gly	Glu	Asn	
							100			105			110			
gag	tat	ttt	agg	gtg	ttt	atg	gag	aat	ttg	atg	aag	aaa	act	aag	caa	384
Glu	Tyr	Phe	Arg	Val	Phe	Met	Glu	Asn	Leu	Met	Lys	Lys	Thr	Lys	Gln	
							115			120			125			
acc	ata	agc	ctc	ttc	aag	gag	gga	aaa	gaa	aga	atg	tat	gag	gag	aat	432
Thr	Ile	Ser	Leu	Phe	Lys	Glu	Gly	Lys	Glu	Arg	Met	Tyr	Glu	Glu	Asn	
							130			135			140			
tct	cag	cct	agg	cga	aac	cta	acc	aaa	ctg	tcc	ctc	atc	ttc	agc	cac	480
Ser	Gln	Pro	Arg	Arg	Asn	Leu	Thr	Lys	Leu	Ser	Leu	Ile	Phe	Ser	His	
							145			150			155			160
atg	ctg	gca	gaa	cta	aaa	gga	atc	ttt	cca	agt	gga	ctc	ttt	cag	gga	528
Met	Leu	Ala	Glu	Leu	Lys	Gly	Ile	Phe	Pro	Ser	Gly	Leu	Phe	Gln	Gly	
							165			170			175			
gac	aca	ttt	cgg	att	act	aaa	gca	gat	gct	gcg	gaa	ttt	tgg	aga	aaa	576
Asp	Thr	Phe	Arg	Ile	Thr	Lys	Ala	Asp	Ala	Ala	Glu	Phe	Trp	Arg	Lys	
							180			185			190			
gct	ttt	ggg	gaa	aag	aca	ata	gtc	cct	tgg	aag	agc	ttt	cga	cag	gct	624
Ala	Phe	Gly	Glu	Lys	Thr	Ile	Val	Pro	Trp	Lys	Ser	Phe	Arg	Gln	Ala	
							195			200			205			
cta	cat	gaa	gtg	cat	ccc	atc	agt	tct	ggg	ctg	gag	gcc	atg	gct	ctg	672
Leu	His	Glu	Val	His	Pro	Ile	Ser	Ser	Gly	Leu	Glu	Ala	Met	Ala	Leu	
							210			215			220			
aaa	tcc	act	att	gat	ctg	acc	tgc	aat	gat	tat	att	tcg	gtt	ttt	gaa	720
Lys	Ser	Thr	Ile	Asp	Leu	Thr	Cys	Asn	Asp	Tyr	Ile	Ser	Val	Phe	Glu	
							225			230			235			240
ttt	gac	atc	ttt	acc	cga	ctc	ttt	cag	ccc	tgg	tcc	tct	ttg	ctc	agg	768
Phe	Asp	Ile	Phe	Thr	Arg	Leu	Phe	Gln	Pro	Trp	Ser	Ser	Leu	Leu	Arg	
							245			250			255			

aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu 260 265 270	816
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro 275 280 285	864
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala 290 295 300	912
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His 305 310 315 320	960
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe 325 330 335	1008
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu 340 345 350	1056
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr 355 360 365	1104
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys 370 375 380	1152
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met 385 390 395 400	1200
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys 405 410 415	1248
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp 420 425 430	1296
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu 435 440 445	1344
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp 450 455 460	1392
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg 465 470 475 480	1440
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val 485 490 495	1488

cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser 500 505 510	1536
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515 520 525	1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530 535 540	1632
cca ccg cct cca gac ccg cca tat tct gtt gga gca gaa tcc cga cct Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545 550 555 560	1680
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565 570 575	1728
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580 585 590	1776
cgg cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595 600 605	1824
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610 615 620	1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625 630 635 640	1920
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645 650 655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala 660 665 670	2016
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675 680 685	2064
ggg gag caa tgt gag ggt gaa gag gac aca gag tac atg act ccc tct Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser 690 695 700	2112
tcc agg cct cta ccg cct ttg gat aca tcc cag agt tca cga gca tgt Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys 705 710 715 720	2160
gat tgc gac cag cag att gat agc tgt acg tat gaa gca atg tat aat Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn 725 730 735	2208

att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu 740 745 750	2256
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu 755 760 765	2304
aat gag gat gat ggg ttt gat gtc cca aag cca cct gtg ccg gcc gtg Asn Glu Asp Asp Gly Phe Asp Val Pro Lys Pro Pro Val Pro Ala Val 770 775 780	2352
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe 785 790 795 800	2400
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly 805 810 815	2448
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg ccg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820 825 830	2496
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala 835 840 845	2544
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu 850 855 860	2592
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile 865 870 875 880	2640
gcc cag aac aac atc gag atg gcc aaa aac atc ctc ccg gaa ttt gtt Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val 885 890 895	2688
tcc att tct cct gcc cat gta gct acc tag Ser Ile Ser Ser Pro Ala His Val Ala Thr 900 905	2721

<210> 256  
 <211> 906  
 <212> PRT  
 <213> artificial

<220>  
 <223> Synthetic Construct

<400> 256

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Thr Gly  
1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His His His His His His His His His Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Tyr Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Tyr Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Phe Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 257  
<211> 2721  
<212> DNA  
<213> artificial

<220>  
<223> c-Cbl Y700F/Y731F/Y774F triple mutant

<220>  
<221> CDS  
<222> (1)..(2718)

<400> 257  
atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc  
Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly

1	5	10	15														
tcc	ggg	ggc	tcg	ggt	tcg	ggt	ggc	ctg	att	ggg	ctc	atg	aag	gac	gcc	96	
Ser	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Gly	Leu	Ile	Gly	Leu	Met	Lys	Asp	Ala	.
20	25												30				
ttc	cag	ccg	cac	cac	cac	cac	cac	cac	ctc	agc	ccc	cac	ccg	ccg	144		
Phe	Gln	Pro	His	His	His	His	His	His	Leu	Ser	Pro	His	Pro	Pro			
35	40											45					
ggg	acg	gtg	gac	aag	aag	atg	gtg	gag	aag	tgc	tgg	aag	ctc	atg	gac	192	
Gly	Thr	Val	Asp	Lys	Lys	Met	Val	Glu	Lys	Cys	Trp	Lys	Leu	Met	Asp		
50	55											60					
aag	gtg	gtg	cg	ttg	tgt	cag	aac	cca	aag	ctg	g	ct	aag	aat	agc	240	
Lys	Val	Val	Arg	Leu	Cys	Gln	Asn	Pro	Lys	Leu	Ala	Leu	Lys	Asn	Ser		
65	70										75		80				
cca	cct	tat	atc	tta	gac	ctg	cta	cca	gat	acc	ta	cag	cat	ctc	cgt	288	
Pro	Pro	Tyr	Ile	Leu	Asp	Leu	Leu	Pro	Asp	Thr	Tyr	Gln	His	Leu	Arg		
85	90										95						
act	atc	ttg	tca	aga	tat	gag	ggg	aag	atg	gag	aca	ctt	gga	gaa	aat	336	
Thr	Ile	Leu	Ser	Arg	Tyr	Glu	Gly	Lys	Met	Glu	Thr	Leu	Gly	Glu	Asn		
100	105										110						
gag	tat	ttt	agg	gtg	ttt	atg	gag	aat	ttg	atg	aag	aaa	act	aag	caa	384	
Glu	Tyr	Phe	Arg	Val	Phe	Met	Glu	Asn	Leu	Met	Lys	Lys	Thr	Lys	Gln		
115	120										125						
acc	ata	agc	ctc	ttc	aag	gag	gga	aaa	gaa	aga	atg	tat	gag	gag	aat	432	
Thr	Ile	Ser	Leu	Phe	Lys	Glu	Gly	Lys	Glu	Arg	Met	Tyr	Glu	Glu	Asn		
130	135										140						
tct	cag	cct	agg	cga	aac	cta	acc	aaa	ctg	tcc	ctc	atc	ttc	agc	cac	480	
Ser	Gln	Pro	Arg	Arg	Asn	Leu	Thr	Lys	Leu	Ser	Leu	Ile	Phe	Ser	His		
145	150										155		160				
atg	ctg	gca	gaa	cta	aaa	gga	atc	ttt	cca	agt	gga	ctc	ttt	cag	gga	528	
Met	Leu	Ala	Glu	Leu	Lys	Gly	Ile	Phe	Pro	Ser	Gly	Leu	Phe	Gln	Gly		
165	170										175						
gac	aca	ttt	cgg	att	act	aaa	gca	gat	gct	g	gaa	ttt	tgg	aga	aaa	576	
Asp	Thr	Phe	Arg	Ile	Thr	Lys	Ala	Asp	Ala	Ala	Glu	Phe	Trp	Arg	Lys		
180	185										190						
gct	ttt	ggg	gaa	aag	aca	ata	gtc	cct	tgg	aag	agc	ttt	cga	cag	gct	624	
Ala	Phe	Gly	Glu	Lys	Thr	Ile	Val	Pro	Trp	Lys	Ser	Phe	Arg	Gln	Ala		
195	200										205						
cta	cat	gaa	gtg	cat	ccc	atc	agt	tct	ggg	ctg	gag	gcc	atg	gct	ctg	672	
Leu	His	Glu	Val	His	Pro	Ile	Ser	Ser	Gly	Leu	Glu	Ala	Met	Ala	Leu		
210	215										220						
aaa	tcc	act	att	gat	ctg	acc	tgc	aat	gat	tat	att	tcg	gtt	ttt	gaa	720	
Lys	Ser	Thr	Ile	Asp	Leu	Thr	Cys	Asn	Asp	Tyr	Ile	Ser	Val	Phe	Glu		
225	230										235		240				
ttt	gac	atc	ttt	acc	cga	ctc	ttt	cag	ccc	tgg	tcc	tct	ttg	ctc	agg	768	
Phe	Asp	Ile	Phe	Thr	Arg	Leu	Phe	Gln	Pro	Trp	Ser	Ser	Leu	Leu	Arg		

245	250	255	
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg			816
Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu			
260	265	270	
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct			864
Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro			
275	280	285	
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct			912
Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala			
290	295	300	
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac			960
Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His			
305	310	315	320
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc			1008
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe			
325	330	335	
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta			1056
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu			
340	345	350	
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat			1104
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr			
355	360	365	
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt			1152
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys			
370	375	380	
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg			1200
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met			
385	390	395	400
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt			1248
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys			
405	410	415	
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat			1296
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp			
420	425	430	
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag			1344
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu			
435	440	445	
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat			1392
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp			
450	455	460	
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg			1440
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg			
465	470	475	480
ccg cct tct cca ttc tcc atg gcc cca caa gct tcc ctt ccc ccg gtg.			1488
Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val			

485	490	495	
cca cca cga ctt gac ctt ctg ccg cag cga gta tgt gtt ccc tca agt Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser 500	505	510	1536
gct tct gct ctt gga act gct tct aag gct gct tct ggc tcc ctt cat Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His 515	520	525	1584
aaa gac aaa cca ttg cca gta cct ccc aca ctt cga gat ctt cca cca Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro 530	535	540	1632
cca ccg cct cca gac cgg cca tat tct gtt gga gca gaa tcc cga cct Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro 545	550	555	1680
caa aga cgc ccc ttg cct tgt aca cca ggc gac tgt ccc tcc aga gac Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp 565	570	575	1728
aaa ctg ccc cct gtc ccc tct agc cgc ctt gga gac tca tgg ctg ccc Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro 580	585	590	1776
cgg cca atc ccc aaa gta cca gta tct gcc cca agt tcc agt gat ccc Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro 595	600	605	1824
tgg aca gga aga gaa tta acc aac cgg cac tca ctt cca ttt tca ttg Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu 610	615	620	1872
ccc tca caa atg gag ccc aga cca gat gtg cct agg ctc gga agc acg Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr 625	630	635	1920
ttc agt ctg gat acc tcc atg agt atg aat agc agc cca tta gta ggt Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly 645	650	655	1968
cca gag tgt gac cac ccc aaa atc aaa cct tcc tca tct gcc aat gcc Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala 660	665	670	2016
att tat tct ctg gct gcc aga cct ctt cct gtg cca aaa ctg cca cct Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro 675	680	685	2064
ggg gag caa tgt gag ggt gaa gag gag aca gag ttc atg act ccc tct Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Phe Met Thr Pro Ser 690	695	700	2112
tcc agg cct cta cgg cct ttg gat aca tcc cag agt tca cga gca tgt Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys 705	710	715	2160
gat tgc gac cag cag att gat agc tgt acg ttt gaa gca atg tat aat Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Phe Glu Ala Met Tyr Asn			2208

725	730	735	
att cag tcc cag gcg cca tct atc acc gag agc agc acc ttt ggt gaa Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu 740	745	750	2256
ggg aat ttg gcc gca gcc cat gcc aac act ggt ccc gag gag tca gaa Gly Asn Leu Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu 755	760	765	2304
aat gag gat gat ggg ttt gat gtc cca aag cca cct gtg ccg gcc gtg Asn Glu Asp Asp Gly Phe Asp Val Pro Lys Pro Pro Val Pro Ala Val 770	775	780	2352
ctg gcc cgc cga act ctc tca gat atc tct aat gcc agc tcc tcc ttt Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe 785	790	795	2400
ggc tgg ttg tct ctg gat ggt gat cct aca aca aat gtc act gaa ggt Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly 805	810	815	2448
tcc caa gtt ccc gag agg cct cca aaa cca ttc ccg ccg aga atc aac Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn 820	825	830	2496
tct gaa cgg aaa gct ggc agc tgt cag caa ggt agt ggt cct gcc gcc Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala 835	840	845	2544
tct gct gcc acc gcc tca cct cag ctc tcc agt gag atc gag aac ctc Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu 850	855	860	2592
atg agt cag ggg tac tcc tac cag gac atc cag aaa gct ttg gtc att Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile 865	870	875	2640
gcc cag aac aac atc gag atg gcc aaa aac atc ctc ccg gaa ttt gtt Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val 885	890	895	2688
tcc att tct tct cct gcc cat gta gct acc tag Ser Ile Ser Ser Pro Ala His Val Ala Thr 900	905		2721

<210> 258  
 <211> 906  
 <212> PRT  
 <213> artificial

<220>  
 <223> Synthetic Construct

<400> 258

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly  
 1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His His His His His His His Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

Pro Pro Ser Pro Phe Ser Met Ala Pro Gln Ala Ser Leu Pro Pro Val  
485 490 495

Pro Pro Arg Leu Asp Leu Leu Pro Gln Arg Val Cys Val Pro Ser Ser  
500 505 510

Ala Ser Ala Leu Gly Thr Ala Ser Lys Ala Ala Ser Gly Ser Leu His  
515 520 525

Lys Asp Lys Pro Leu Pro Val Pro Pro Thr Leu Arg Asp Leu Pro Pro  
530 535 540

Pro Pro Pro Pro Asp Arg Pro Tyr Ser Val Gly Ala Glu Ser Arg Pro  
545 550 555 560

Gln Arg Arg Pro Leu Pro Cys Thr Pro Gly Asp Cys Pro Ser Arg Asp  
565 570 575

Lys Leu Pro Pro Val Pro Ser Ser Arg Leu Gly Asp Ser Trp Leu Pro  
580 585 590

Arg Pro Ile Pro Lys Val Pro Val Ser Ala Pro Ser Ser Ser Asp Pro  
595 600 605

Trp Thr Gly Arg Glu Leu Thr Asn Arg His Ser Leu Pro Phe Ser Leu  
610 615 620

Pro Ser Gln Met Glu Pro Arg Pro Asp Val Pro Arg Leu Gly Ser Thr  
625 630 635 640

Phe Ser Leu Asp Thr Ser Met Ser Met Asn Ser Ser Pro Leu Val Gly  
645 650 655

Pro Glu Cys Asp His Pro Lys Ile Lys Pro Ser Ser Ser Ala Asn Ala  
660 665 670

Ile Tyr Ser Leu Ala Ala Arg Pro Leu Pro Val Pro Lys Leu Pro Pro  
675 680 685

Gly Glu Gln Cys Glu Gly Glu Glu Asp Thr Glu Phe Met Thr Pro Ser  
690 695 700

Ser Arg Pro Leu Arg Pro Leu Asp Thr Ser Gln Ser Ser Arg Ala Cys  
705 710 715 720

Asp Cys Asp Gln Gln Ile Asp Ser Cys Thr Phe Glu Ala Met Tyr Asn  
725 730 735

Ile Gln Ser Gln Ala Pro Ser Ile Thr Glu Ser Ser Thr Phe Gly Glu  
740 745 750

Gly Asn Leu Ala Ala Ala His Ala Asn Thr Gly Pro Glu Glu Ser Glu  
755 760 765

Asn Glu Asp Asp Gly Phe Asp Val Pro Lys Pro Pro Val Pro Ala Val  
770 775 780

Leu Ala Arg Arg Thr Leu Ser Asp Ile Ser Asn Ala Ser Ser Ser Phe  
785 790 795 800

Gly Trp Leu Ser Leu Asp Gly Asp Pro Thr Thr Asn Val Thr Glu Gly  
805 810 815

Ser Gln Val Pro Glu Arg Pro Pro Lys Pro Phe Pro Arg Arg Ile Asn  
820 825 830

Ser Glu Arg Lys Ala Gly Ser Cys Gln Gln Gly Ser Gly Pro Ala Ala  
835 840 845

Ser Ala Ala Thr Ala Ser Pro Gln Leu Ser Ser Glu Ile Glu Asn Leu  
850 855 860

Met Ser Gln Gly Tyr Ser Tyr Gln Asp Ile Gln Lys Ala Leu Val Ile  
865 870 875 880

Ala Gln Asn Asn Ile Glu Met Ala Lys Asn Ile Leu Arg Glu Phe Val  
885 890 895

Ser Ile Ser Ser Pro Ala His Val Ala Thr  
900 905

<210> 259

<211> 1443

<212> DNA

<213> artificial

<220>

<223> c-Cbl480 mutant

<220>

<221> CDS

<222> (1)..(1440)

<400> 259

atg gcc ggc aac gtg aag aag agc tct ggg gcc ggg ggc ggc acg ggc

48

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Gly Thr Gly			
1 5 10 15			
tcc ggg ggc tcg ggt tcg ggt ggc ctg att ggg ctc atg aag gac gac	96		
Ser Gly Gly Ser Gly Gly Leu Ile Gly Leu Met Lys Asp Ala			
20 25 30			
ttc cag ccg cac cac cac cac cac ctc agc ccc cac ccg ccg	144		
Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro			
35 40 45			
ggg acg gtg gac aag aag atg gtg gag aag tgc tgg aag ctc atg gac	192		
Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp			
50 55 60			
aag gtg gtg cggttgcgttgtcagaacccaaagctggcgctaaagaaatagc	240		
Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser			
65 70 75 80			
cca cct tat atc tta gac ctg cta cca gat acc tac cag cat ctc cgt	288		
Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg			
85 90 95			
act atc ttg tca aga tat gag ggg aag atg gag aca ctt gga gaa aat	336		
Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn			
100 105 110			
gag tat ttt agg gtg ttt atg gag aat ttg atg aag aaa act aag caa	384		
Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln			
115 120 125			
acc ata agc ctc ttc aag gag gga aaa gaa aga atg tat gag gag aat	432		
Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn			
130 135 140			
tct cag cct agg cga aac cta acc aaa ctg tcc ctc atc ttc agc cac	480		
Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His			
145 150 155 160			
atg ctg gca gaa cta aaa gga atc ttt cca agt gga ctc ttt cag gga	528		
Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly			
165 170 175			
gac aca ttt cgg att act aaa gca gat gct gcg gaa ttt tgg aga aaa	576		
Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys			
180 185 190			
gct ttt ggg gaa aag aca ata gtc cct tgg aag agc ttt cga cag gct	624		
Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala			
195 200 205			
cta cat gaa gtg cat ccc atc agt tct ggg ctg gag gcc atg gct ctg	672		
Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu			
210 215 220			
aaa tcc act att gat ctg acc tgc aat gat tat att tcg gtt ttt gaa	720		
Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu			
225 230 235 240			
ttt gac atc ttt acc cga ctc ttt cag ccc tgg tcc tct ttg ctc agg	768		

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg			
245	250	255	
aat tgg aac agc ctt gct gta act cat cct ggc tac atg gct ttt ttg			816
Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu			
260	265	270	
acg tat gac gaa gtg aaa gct cgg ctc cag aaa ttc att cac aaa cct			864
Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro			
275	280	285	
ggc agt tat atc ttc cgg ctg agc tgt act cgt ctg ggt cag tgg gct			912
Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala			
290	295	300	
att ggg tat gtt act gct gat ggg aac att ctc cag aca atc cct cac			960
Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His			
305	310	315	320
aat aaa cct ctc ttc caa gca ctg att gat ggc ttc agg gaa ggc ttc			1008
Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe			
325	330	335	
tat ttg ttt cct gat gga cga aat cag aat cct gat ctg act ggc tta			1056
Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu			
340	345	350	
tgt gaa cca act ccc caa gac cat atc aaa gtg acc cag gaa caa tat			1104
Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr			
355	360	365	
gaa tta tac tgt gag atg ggc tcc aca ttc caa cta tgt aaa ata tgt			1152
Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys			
370	375	380	
gct gaa aat gat aag gat gta aag att gag ccc tgt gga cac ctc atg			1200
Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met			
385	390	395	400
tgc aca tcc tgt ctt aca tcc tgg cag gaa tca gaa ggt cag ggc tgt			1248
Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys			
405	410	415	
cct ttc tgc cga tgt gaa att aaa ggt act gaa ccc atc gtg gta gat			1296
Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp			
420	425	430	
ccg ttt gat cct aga ggg agt ggc agc ctg ttg agg caa gga gca gag			1344
Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu			
435	440	445	
gga gct ccc tcc cca aat tat gat gat gat gat gaa cga gct gat			1392
Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Glu Arg Ala Asp			
450	455	460	
gat act ctc ttc atg atg aag gaa ttg gct ggt gcc aag gtg gaa cgg			1440
Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg			
465	470	475	480
tag			1443

<210> 260  
<211> 480  
<212> PRT  
<213> artificial

<220>  
<223> Synthetic Construct

<400> 260

Met Ala Gly Asn Val Lys Lys Ser Ser Gly Ala Gly Gly Thr Gly  
1 5 10 15

Ser Gly Gly Ser Gly Ser Gly Leu Ile Gly Leu Met Lys Asp Ala  
20 25 30

Phe Gln Pro His His His His His His Leu Ser Pro His Pro Pro  
35 40 45

Gly Thr Val Asp Lys Lys Met Val Glu Lys Cys Trp Lys Leu Met Asp  
50 55 60

Lys Val Val Arg Leu Cys Gln Asn Pro Lys Leu Ala Leu Lys Asn Ser  
65 70 75 80

Pro Pro Tyr Ile Leu Asp Leu Leu Pro Asp Thr Tyr Gln His Leu Arg  
85 90 95

Thr Ile Leu Ser Arg Tyr Glu Gly Lys Met Glu Thr Leu Gly Glu Asn  
100 105 110

Glu Tyr Phe Arg Val Phe Met Glu Asn Leu Met Lys Lys Thr Lys Gln  
115 120 125

Thr Ile Ser Leu Phe Lys Glu Gly Lys Glu Arg Met Tyr Glu Glu Asn  
130 135 140

Ser Gln Pro Arg Arg Asn Leu Thr Lys Leu Ser Leu Ile Phe Ser His  
145 150 155 160

Met Leu Ala Glu Leu Lys Gly Ile Phe Pro Ser Gly Leu Phe Gln Gly  
165 170 175

Asp Thr Phe Arg Ile Thr Lys Ala Asp Ala Ala Glu Phe Trp Arg Lys  
180 185 190

Ala Phe Gly Glu Lys Thr Ile Val Pro Trp Lys Ser Phe Arg Gln Ala  
195 200 205

Leu His Glu Val His Pro Ile Ser Ser Gly Leu Glu Ala Met Ala Leu  
210 215 220

Lys Ser Thr Ile Asp Leu Thr Cys Asn Asp Tyr Ile Ser Val Phe Glu  
225 230 235 240

Phe Asp Ile Phe Thr Arg Leu Phe Gln Pro Trp Ser Ser Leu Leu Arg  
245 250 255

Asn Trp Asn Ser Leu Ala Val Thr His Pro Gly Tyr Met Ala Phe Leu  
260 265 270

Thr Tyr Asp Glu Val Lys Ala Arg Leu Gln Lys Phe Ile His Lys Pro  
275 280 285

Gly Ser Tyr Ile Phe Arg Leu Ser Cys Thr Arg Leu Gly Gln Trp Ala  
290 295 300

Ile Gly Tyr Val Thr Ala Asp Gly Asn Ile Leu Gln Thr Ile Pro His  
305 310 315 320

Asn Lys Pro Leu Phe Gln Ala Leu Ile Asp Gly Phe Arg Glu Gly Phe  
325 330 335

Tyr Leu Phe Pro Asp Gly Arg Asn Gln Asn Pro Asp Leu Thr Gly Leu  
340 345 350

Cys Glu Pro Thr Pro Gln Asp His Ile Lys Val Thr Gln Glu Gln Tyr  
355 360 365

Glu Leu Tyr Cys Glu Met Gly Ser Thr Phe Gln Leu Cys Lys Ile Cys  
370 375 380

Ala Glu Asn Asp Lys Asp Val Lys Ile Glu Pro Cys Gly His Leu Met  
385 390 395 400

Cys Thr Ser Cys Leu Thr Ser Trp Gln Glu Ser Glu Gly Gln Gly Cys  
405 410 415

Pro Phe Cys Arg Cys Glu Ile Lys Gly Thr Glu Pro Ile Val Val Asp  
420 425 430

Pro Phe Asp Pro Arg Gly Ser Gly Ser Leu Leu Arg Gln Gly Ala Glu  
435 440 445

Gly Ala Pro Ser Pro Asn Tyr Asp Asp Asp Asp Asp Glu Arg Ala Asp  
450 455 460

Asp Thr Leu Phe Met Met Lys Glu Leu Ala Gly Ala Lys Val Glu Arg  
465 470 475 480

<210> 261  
<211> 2721  
<212> DNA  
<213> Homo sapiens

<400> 261  
atggccggca acgtgaagaa gagctctggg gccggggcg gcacgggctc cgggggctcg 60  
ggttcgggtg gcctgattgg gctcatgaag gacgccttcc agccgcacca ccaccaccac 120  
caccacctca gcccccaccc gccggggacg gtggacaaga agatggtgga gaagtgctgg 180  
aagctcatgg acaaggtggt gcgggtgtgt cagaacccaa agctggcgct aaagaatagc 240  
ccaccttata tcttagacct gctaccagat acctaccagc atctccgtac tatcttgtca 300  
agatatgagg ggaagatgga gacacttgga gaaaatgagt attttagggt gtttatggag 360  
aattttagatga agaaaactaa gcaaaccata agcctttca aggagggaaa agaaagaatg 420  
tatgaggaga attctcagcc taggcgaaac ctaaccaaac tgtccctcat cttagccac 480  
atgctggcag aactaaaagg aatcttcca agtggactct ttcagggaga cacattcgg 540  
attactaaag cagatgctgc ggaattttgg agaaaagctt ttggggaaaa gacaatagtc 600  
ccttggaga gcttcgaca ggctctacat gaagtgcac ccacgttc tggctggag 660  
gccatggctc taaaatccac tattgatctg acctgcaatg attatatttc gtttttggaa 720  
tttgacatct ttacccgact cttcagccc tggcctctt tgctcaggaa ttggAACAGC 780  
cttgctgtaa ctcatcctgg ctacatggct ttttgacgt atgacgaagt gaaagctcg 840  
ctccagaaaat tcattcacaa acctggcagt tatacttcc ggctgagctg tactcgtctg 900  
ggtcagtggg ctattggta tgttactgct gatggaaaca ttctccagac aatccctcac 960  
aataaacctc tcttccaagc actgattgat ggcttcaggg aaggcttcta tttgtttcct 1020  
gatggacgaa atcagaatcc tgatctgact ggcttatgtg aaccaactcc ccaagaccat 1080  
atcaaagtga cccaggaaca atatgaatta tactgtgaga tggctccac attccaacta 1140  
tgtaaaaatgtgctgaaaa tgataaggat gtaaagattg agccctgtgg acacctcatg 1200  
tgcacatcct gtcttacatc ctggcaggaa tcagaaggc agggctgtcc tttctgccga 1260

tgtgaaat ta aaggtactga acccatcgta gtagatccgt ttgatcctag agggagtgcc 1320  
agcctgttga ggcaaggagc agagggagct ccctcccaa attatgtatgatgatgat 1380  
gaacgagctg atgatactct cttcatgtatg aaggaattgg ctggtgccaa ggtgaaacgg 1440  
ccgccttctc cattctccat ggccccacaa gcttcccttc ccccggtgcc accacgactt 1500  
gaccttctgc cgcaagcgagt atgtgttccc tcaagtgttctt ctgctcttgg aactgcttct 1560  
aaggctgctt ctggctccat tcataaagac aaaccattgc cagtaacctcc cacacttcga 1620  
gatcttccac caccaccgccc tccagaccgg ccatattctg ttggagcaga atcccgacct 1680  
caaagacgcc ccttgccttg tacaccaggc gactgtccct ccagagacaa actgccccct 1740  
gtccccctcta gcccgccttgg agactcatgg ctgccccggc caatccccaa agtaccagta 1800  
tctgccccaa gttccagtga tccctggaca ggaagagaat taaccaaccg gcactcactt 1860  
ccattttcat tgccctcaca aatggagccc agaccagatg tgcctaggct cggaagcacg 1920  
ttcagttctgg atacctccat gagtatgaat agcagcccat tagtaggtcc agagtgtgac 1980  
caccccaaaa tcaaacccttc ctcatctgcc aatgccattt attctctggc tgccagacct 2040  
cttcctgtgc caaaaactgcc acctggggag caatgtgagg gtgaagagga cacagagtac 2100  
atgactccct cttccaggcc tctacggcct ttggatacat cccagagttc acgagcatgt 2160  
gattgcgacc agcagattga tagctgtacg tatgaagcaa tgtataatat tcagtcctcag 2220  
gcgccatcta tcaccgagag cagcacctt ggtgaaggaa atttggccgc agcccatgcc 2280  
aacactggtc ccgaggagtc agaaaatgag gatgatgggt atgatgtccc aaagccacct 2340  
gtgccggccg tgctggcccg ccgaactctc tcagatatct ctaatgccag ctccctctt 2400  
ggctgggtgt ctctggatgg tgatcctaca acaaattgtca ctgaaggttc ccaagttccc 2460  
gagaggcctc caaaaaccatt cccgcggaga atcaactctg aacggaaagc tggcagctgt 2520  
cagcaaggta gtggcctgc cgcctctgct gccaccgcct cacctcagct ctccagtgag 2580  
atcgagaacc tcatgagtca ggggtactcc taccaggaca tccagaaagc tttggtcatt 2640  
gcccagaaca acatcgagat ggccaaaaac atcctccggg aatttggttc catttcttct 2700  
cctgcccattg tagctaccta g 2721